

Amendments to the Claims:

The following listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Currently Amended) A method of repressing ~~expression~~ transcription of a coding sequence of interest in a transgenic plant, comprising:

a) introducing into a plant:

i) a first chimeric nucleotide sequence comprising a first regulatory element in operative association with said coding sequence of interest, and a controlling sequence; and

ii) a second chimeric nucleotide sequence comprising a second regulatory element in operative association with a nucleotide sequence encoding a histone deacetylase fused with a DNA binding protein, said DNA binding protein interacting with said controlling sequence, to produce said transgenic plant; and

b) growing said transgenic plant;

wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of:

AtRPD3A, a nucleotide sequence that hybridizes to *AtRPD3A* under a hybridization condition,

AtRPD3B, a nucleotide sequence that hybridizes to *AtRPD3B* under a hybridization condition,

AtHD2A, a nucleotide sequence that hybridizes to *AtHD2A* under a hybridization condition,

AtHD2B, a nucleotide sequence that hybridizes to *AtHD2B* under a hybridization condition,

nucleotides 1-1807 of SEQ ID NO:1, a nucleotide sequence that hybridizes to nucleotides 1-1807 of SEQ ID NO:1 under a hybridization condition,

nucleotides 142-1644 of SEQ ID NO:1, a nucleotide sequence that hybridizes to nucleotides 142-1644 of SEQ ID NO:1 under a hybridization condition,

nucleotides 1-1800 of SEQ ID NO:3, a nucleotide sequence that hybridizes to nucleotides 1-1800 of SEQ ID NO:3 under a hybridization condition,

nucleotides 121-1533 of SEQ ID NO:3, a nucleotide sequence that hybridizes to nucleotides 121-1533 of SEQ ID NO:3 under a hybridization condition,

nucleotides 1-939 of SEQ ID NO:5, a nucleotide sequence that hybridizes to nucleotides 1-939 of SEQ ID NO:5 under a hybridization condition,

nucleotides 49-783 of SEQ ID NO:5, a nucleotide sequence that hybridizes to nucleotides 49-783 of SEQ ID NO:5 under a hybridization condition,

nucleotides 49-681 of SEQ ID NO:5, a nucleotide sequence that hybridizes to nucleotides 49-681 of SEQ ID NO:5 under a hybridization condition,

nucleotides 49-534 of SEQ ID NO:5, a nucleotide sequence that hybridizes to nucleotides 49-534 of SEQ ID NO:5 under a hybridization condition,

nucleotides 1-1212 of SEQ ID NO:7, a nucleotide sequence that hybridizes to nucleotides 1-1212 of SEQ ID NO:7 under a hybridization condition, and

nucleotides 61-975 of SEQ ID NO:7, a nucleotide sequence that hybridizes to nucleotides 61-975 of SEQ ID NO:7 under a hybridization condition;

wherein each said hybridization condition is selected from the group consisting of:

hybridization in 4XSSC at 65°C, followed by washing in 0.1XSSC at 65°C for an hour,

hybridization in 50% formamide and 4XSSC at 42°C, followed by washing in 0.1XSSC at 65°C for an hour, and

hybridization in 0.5 M Na₂HPO₄ (pH 7.2), 7% SDS, and 1mM EDTA at 65°C, followed by washing for 15 minutes in 2 x SSC with 0.1% SDS at room temperature, then washing twice for 20 minutes in 0.1 x SSC, 0.1% SDS at 65°C; and

wherein said nucleotide sequence that hybridizes encodes a product that exhibits ~~repression~~ transcription of gene expression activity.

2. (Original) The method of claim 1 wherein the step of introducing comprises sequentially transforming said plant with said first, and said second, chimeric nucleotide sequence, or co-transforming said plant with said first and said second chimeric nucleotide sequences.

3. (Original) The method of claim 1, wherein the step of introducing comprises transforming a first plant with said first chimeric nucleotide sequence, and transforming a second plant with said second chimeric nucleotide sequence, followed by a step of crossing said first and said second plant, to produce said transgenic plant.

4. (Canceled)

5. (Original) The method of claim 1 wherein said first chimeric nucleotide sequence and the second chimeric nucleotide sequence, within said step of introducing, are contiguous within one construct.

6. (Original) The method of claim 1 wherein the first chimeric nucleotide sequence and the second chimeric nucleotide sequence, within said step of introducing, are separate constructs.

7. (Original) The method of claim 1 wherein said DNA binding protein, within the step of introducing, is selected from the group consisting of GAL4, AP2 domain proteins,

APETALA2, PRbox binding protein, CCAAT-box binding proteins, LEC1, BNM3, Pti4, and PICKLE.

8. (Original) The method of claim 1 wherein said first and said second regulatory region, within said step of introducing, are selected from the group consisting of constitutive, tissue specific, developmentally-regulated, and inducible regulatory elements.

9. (Currently Amended) An isolated nucleotide sequence, selected from the group consisting of:

SEQ ID NO:3, ~~SEQ ID NO:5, or SEQ ID NO:7,~~

a nucleotide sequence that hybridizes to SEQ ID NO:3 under a hybridization condition,

SEQ ID NO:5, or

a nucleotide sequence that hybridizes to SEQ ID NO:5 under a hybridization condition,

SEQ ID NO:7,

a nucleotide sequence that hybridizes to SEQ ID NO:7 under a hybridization condition,

nucleotides 1-1800 of SEQ ID NO:3,

a nucleotide sequence that hybridizes to nucleotides 1-1800 of SEQ ID NO:3 under a hybridization condition,

nucleotides 121-1533 of SEQ ID NO:3,

a nucleotide sequence that hybridizes to nucleotides 121-1533 of SEQ ID NO:3 under a hybridization condition,

nucleotides 1-939 of SEQ ID NO:5,

a nucleotide sequence that hybridizes to nucleotides 1-939 of SEQ ID NO:5 under a hybridization condition,

nucleotides 49-783 of SEQ ID NO:5,

a nucleotide sequence that hybridizes to nucleotides 49-783 of SEQ ID NO:5
under a hybridization condition,

nucleotides 49-681 of SEQ ID NO:5,

a nucleotide sequence that hybridizes to nucleotides 49-681 of SEQ ID NO:5
under a hybridization condition,

nucleotides 49-534 of SEQ ID NO:5,

a nucleotide sequence that hybridizes to nucleotides 49-534 of SEQ ID NO:5
under a hybridization condition,

nucleotides 1-1212 of SEQ ID NO:7,

a nucleotide sequence that hybridizes to nucleotides 1-1212 of SEQ ID NO:7
under a hybridization condition,

nucleotides 61-975 of SEQ ID NO:7, and

a nucleotide sequence that hybridizes to nucleotides 61-975 of SEQ ID NO:7
under a hybridization condition;

wherein each said hybridization condition is selected from the group
consisting of:

hybridization in 4XSSC at 65°C, followed by washing in 0.1XSSC at
65°C for an hour,

hybridization in 50% formamide and 4XSSC at 42°C, followed by
washing in 0.1XSSC at 65°C for an hour, and

hybridization in 0.5 M Na₂HPO₄ (pH 7.2), 7% SDS, and 1 mM EDTA
at 65°C, followed by washing for 15 minutes in 2 x SSC with 0.1% SDS at room temperature,
then twice washing for 20 minutes in 0.1 x SSC, 0.1% SDS at 65°C; and

wherein said nucleotide sequence that hybridizes encodes a product that exhibits ~~repression~~ transcription of gene expression activity.

10. (Canceled)
11. (Original) A chimeric construct comprising a regulatory element in operative association with said isolated nucleotide sequence of claim 9.
12. (Original) The chimeric construct of claim 11 further comprising a nucleotide sequence encoding a DNA binding protein.
13. (Original) A vector comprising said chimeric construct of claim 12.
14. (Previously Presented) A transgenic plant cell produced by the method of claim 1.
15. (Previously Presented) A transgenic plant produced by the method of claim 1.
16. (Original) A transgenic seed produced by the method of claim 1.
17. (Original) A transgenic plant comprising said isolated nucleotide sequence as defined by claim 9.
18. (Original) A transgenic plant cell comprising said isolated nucleotide sequence as defined by claim 9.
19. (Original) A transgenic seed comprising said isolated nucleotide sequence as defined by claim 9.
- 20-30. (Canceled)
31. (Previously Presented) An isolated nucleotide sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:5 and SEQ ID NO:7.
32. (Previously Presented) The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: AtRPD3A, AtRPD3B, AtHD2A, and AtHD2B.

33. (Previously Presented) The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of nucleotides 1-1807 of SEQ ID NO:1 and nucleotides 142-1644 of SEQ ID NO:1.

34. (Previously Presented) The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: nucleotides 1-1800 of SEQ ID NO:3 and nucleotides 121-1533 of SEQ ID NO:3.

35. (Previously Presented) The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: nucleotides 1-939 of SEQ ID NO:5; nucleotides 49-783 of SEQ ID NO:5; nucleotides 49-681 of SEQ ID NO:5; and nucleotides 49-534 of SEQ ID NO:5.

36. (Currently Amended) The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: nucleotides 1-1212 of SEQ ID NO:7; and a nucleotides 61-975 of SEQ ID NO:7; ~~nucleotides 61-855 of SEQ ID NO:7; and nucleotides 61-655 of SEQ ID NO:7.~~

37. (Previously Presented) The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: a nucleotide sequence that hybridizes to AtRPD3A, a nucleotide sequence that hybridizes to AtRPD3B, a nucleotide sequence that hybridizes to AtHD2A, and a nucleotide sequence that hybridizes to AtHD2B.

38. (Previously Presented) The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: a nucleotide sequence that hybridizes to nucleotides 1-1807 of SEQ ID NO:1 and a nucleotide sequence that hybridizes to nucleotides 142-1644 of SEQ ID NO:1.

39. (Previously Presented) The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: a nucleotide

sequence that hybridizes to nucleotides 1-1800 of SEQ ID NO:3 and a nucleotide sequence that hybridizes to nucleotides 121-1533 of SEQ ID NO:3.

40. (Previously Presented) The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: a nucleotide sequence that hybridizes to nucleotides 1-939 of SEQ ID NO:5; a nucleotide sequence that hybridizes to nucleotides 49-783 of SEQ ID NO:5; a nucleotide sequence that hybridizes to nucleotides 49-681 of SEQ ID NO:5; and a nucleotide sequence that hybridizes to nucleotides 49-534 of SEQ ID NO:5.

41. (Currently Amended) The method of claim 1, wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of: a nucleotide sequence that hybridizes to nucleotides 1-1212 of SEQ ID NO:7; and a nucleotide sequence that hybridizes to nucleotides 61-975 of SEQ ID NO:7; ~~a nucleotide sequence that hybridizes to nucleotides 61-855 of SEQ ID NO:7; and a nucleotide sequence that hybridizes to nucleotides 61-655 of SEQ ID NO:7.~~

42. (Currently Amended) The isolated nucleotide ~~sequences~~ sequence of claim 9, wherein said nucleotide sequence comprises SEQ ID NO:3.

43. (Currently Amended) The isolated nucleotide sequence ~~sequences~~ of claim 9, wherein said nucleotide sequence comprises SEQ ID NO:5.

44. (Currently Amended) The isolated nucleotide sequence ~~sequences~~ of claim 9, wherein said nucleotide sequence comprises SEQ ID NO:7.

45. (Currently Amended) The isolated nucleotide sequence ~~sequences~~ of claim 9, wherein said nucleotide sequence comprises nucleotides 121-1533 of SEQ ID NO:3.

46. (Currently Amended) The isolated nucleotide sequence ~~sequences~~ of claim 9, wherein said nucleotide sequence comprises nucleotides 1-939 of SEQ ID NO:5.

47. (Currently Amended) The isolated nucleotide ~~sequence sequences~~ of claim 9, wherein said nucleotide sequence comprises nucleotides 49-783 of SEQ ID NO:5.

48. (Currently Amended) The isolated nucleotide ~~sequence sequences~~ of claim 9, wherein said nucleotide sequence comprises nucleotides 49-681 of SEQ ID NO:5.

49. (Currently Amended) The isolated nucleotide ~~sequences sequence~~ of claim 9, wherein said nucleotide sequence comprises nucleotides 49-534 of SEQ ID NO:5.

50. (Canceled)

51. (Currently Amended) The isolated nucleotide ~~sequences sequence~~ of claim 9, wherein said nucleotide sequence comprises nucleotides 1-1212 of SEQ ID NO:7.

52. (Currently Amended) The isolated nucleotide ~~sequences sequence~~ of claim 9, wherein said nucleotide sequence comprises nucleotides 61-975 of SEQ ID NO:7.

53-56. (Canceled)